

RAW SEQUENCE LISTING

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Application Serial Number: 10/540,971
Source: PCT
Date Processed by STIC: 7-11-05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 07/11/2005

PATENT APPLICATION: US/10/540,971

TIME: 15:05:25

Input Set : A:\01640393aa.txt

Output Set: N:\CRF4\07112005\J540971.raw

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3 <110> APPLICANT: Whaley, Cory M.
4     Wilson, Henry P.
5     Westwood, James H.
7 <120> TITLE OF INVENTION: Gene Encoding Resistance to Acetolactate Synthase-Inhibiting
8     Herbicides
10 <130> FILE REFERENCE: 01640393aa
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/540,971
C--> 12 <141> CURRENT FILING DATE: 2005-06-27
12 <150> PRIOR APPLICATION NUMBER: US 60/438,801
13 <151> PRIOR FILING DATE: 2003-01-09
15 <150> PRIOR APPLICATION NUMBER: PCTUS04/00363
16 <151> PRIOR FILING DATE: 2004-01-09
18 <160> NUMBER OF SEQ ID NOS: 8
20 <170> SOFTWARE: PatentIn version 3.2
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1846
24 <212> TYPE: DNA
25 <213> ORGANISM: Amaranthus hybridus
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32 cccagaaaag gttgcgatgt tctcggtgaa gctcttgaaac gtgaagggtg taccgatgtt      180
34 tttgcttacc ctggtggagc atccatggaa attcatcaag ctcttactcg ttctaataatc      240
36 attagaaatg ttcttcctcg acatgaacaa ggtgggggtt tcgctgctga aggctacgct      300
38 cgtgctactg gacgcgttgg agtttgtatt gccacttctg gtccagggtg tactaatctt      360
40 gtttctgggt ttgctgatgc acttcttgac tcagtccttc ttgtcgccat tactgggcaa      420
42 gttccccggc gtatgattgg tactgatgct tttcaagaga ctccaattgt tgaggtaact      480
44 cgatccatta ccaagcataa ttatttggtg ttagatgttg aggatattcc tagaattggt      540
46 aaggaagctt tcttttttagc taattctggt agacctggac ctgttttgat tgatattcct      600
48 aaagatattc agcaacaatt agttgttcct aattgggaac agcccattaa attgggtggg      660
50 tatctttcta ggttgccata acccacttat tctgctaata aagagggact tcttgatcaa      720
52 attgtaaggt tagtggtgga gtctaagaga cctgtgctgt atactggagg tgggtggttg      780
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56 ttaatggggt tgggggcttt cccttgctact gatgatttat ctcttcatat gttgggaatg      900
58 cacgggactg tgtacgcgaa ttacgcgggt gataaggccg atttggtgct tgcttttggg      960
60 gttaggtttg atgaacgagt gactggtaag ctcgaggcgt ttgctagccg ggctaagatt      1020
62 gtgcacatcg atatcgattc tgctgaaatc ggggaagaata agcaacctca tgtgtcgatt      1080
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68 cctttgagtt ttaagacttt cggggatgca attcctccgc aatacgccat tcaggttctt      1260
70 gacgagttga cgaagggcga tgcggttgta agtactggtg ttgggcagca ccaaagtgtg      1320
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76 gttgtagaca ttgatgggga tgggagtttt atcatgaatg ttcaagagtt ggctacgatt 1500
78 agggtagaga atctcccggt taaaatcatg ctcttgaaca atcaacattt aggtatggtt 1560
80 gttcaatggg aagatcgatt ttacaaagct aaccgggcac atacatacct cggaatcct 1620
82 tccaattctt ccgaaatctt cccggatatg ctcaaatttg ctgaagcatg tgatatacca 1680
84 gcagcccgtg ttaccaaggt gagcgattta agggctgcaa ttcaaacaat gttggatact 1740
86 ccaggaccgt atctgctgga tgtaatcgta ccacatcagg agcatgtgct gcctatgatc 1800
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92 <211> LENGTH: 614
93 <212> TYPE: PRT
94 <213> ORGANISM: Amaranthus hybridus
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99 1 5 10 15
102 Thr Gln Ser Pro Ser Ser Leu Thr Asp Asp Lys Pro Ser Ser Phe Val
103 20 25 30
106 Ser Arg Phe Ser Pro Glu Glu Pro Arg Lys Gly Cys Asp Val Leu Val
107 35 40 45
110 Glu Ala Leu Glu Arg Glu Gly Val Thr Asp Val Phe Ala Tyr Pro Gly
111 50 55 60
114 Gly Ala Ser Met Glu Ile His Gln Ala Leu Thr Arg Ser Asn Ile Ile
115 65 70 75 80
118 Arg Asn Val Leu Pro Arg His Glu Gln Gly Gly Val Phe Ala Ala Glu
119 85 90 95
122 Gly Tyr Ala Arg Ala Thr Gly Arg Val Gly Val Cys Ile Ala Thr Ser
123 100 105 110
126 Gly Pro Gly Ala Thr Asn Leu Val Ser Gly Leu Ala Asp Ala Leu Leu
127 115 120 125
130 Asp Ser Val Pro Leu Val Ala Ile Thr Gly Gln Val Pro Arg Arg Met
131 130 135 140
134 Ile Gly Thr Asp Ala Phe Gln Glu Thr Pro Ile Val Glu Val Thr Arg
135 145 150 155 160
138 Ser Ile Thr Lys His Asn Tyr Leu Val Leu Asp Val Glu Asp Ile Pro
139 165 170 175
142 Arg Ile Val Lys Glu Ala Phe Phe Leu Ala Asn Ser Gly Arg Pro Gly
143 180 185 190
146 Pro Val Leu Ile Asp Ile Pro Lys Asp Ile Gln Gln Gln Leu Val Val
147 195 200 205
150 Pro Asn Trp Glu Gln Pro Ile Lys Leu Gly Gly Tyr Leu Ser Arg Leu
151 210 215 220
154 Pro Lys Pro Thr Tyr Ser Ala Asn Glu Glu Gly Leu Leu Asp Gln Ile
155 225 230 235 240
158 Val Arg Leu Val Gly Glu Ser Lys Arg Pro Val Leu Tyr Thr Gly Gly
159 245 250 255
162 Gly Cys Leu Asn Ser Ser Glu Glu Leu Arg Lys Phe Val Glu Leu Thr
163 260 265 270
166 Gly Ile Pro Val Ala Ser Thr Leu Met Gly Leu Gly Ala Phe Pro Cys
167 275 280 285
170 Thr Asp Asp Leu Ser Leu His Met Leu Gly Met His Gly Thr Val Tyr

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174 Ala Asn Tyr Ala Val Asp Lys Ala Asp Leu Leu Leu Ala Phe Gly Val
175 305      310      315      320
178 Arg Phe Asp Glu Arg Val Thr Gly Lys Leu Glu Ala Phe Ala Ser Arg
179      325      330      335
182 Ala Lys Ile Val His Ile Asp Ile Asp Ser Ala Glu Ile Gly Lys Asn
183      340      345      350
186 Lys Gln Pro His Val Ser Ile Cys Gly Asp Val Lys Val Ala Leu Gln
187      355      360      365
190 Gly Leu Asn Lys Ile Leu Glu Ser Arg Lys Gly Lys Val Lys Leu Asp
191      370      375      380
194 Phe Ser Asn Trp Arg Glu Leu Asn Glu Gln Lys Lys Lys Phe Pro
195 385      390      395      400
198 Leu Ser Phe Lys Thr Phe Gly Asp Ala Ile Pro Pro Gln Tyr Ala Ile
199      405      410      415
202 Gln Val Leu Asp Glu Leu Thr Lys Gly Asp Ala Val Val Ser Thr Gly
203      420      425      430
206 Val Gly Gln His Gln Met Trp Ala Ala Gln Phe Tyr Lys Tyr Arg Asn
207      435      440      445
210 Pro Arg Gln Trp Leu Thr Ser Gly Gly Leu Gly Ala Met Gly Phe Gly
211      450      455      460
214 Leu Pro Ala Ala Ile Gly Ala Ala Val Ala Arg Pro Asp Ala Val Val
215 465      470      475      480
218 Val Asp Ile Asp Gly Asp Gly Ser Phe Ile Met Asn Val Gln Glu Leu
219      485      490      495
222 Ala Thr Ile Arg Val Glu Asn Leu Pro Val Lys Ile Met Leu Leu Asn
223      500      505      510
226 Asn Gln His Leu Gly Met Val Val Gln Trp Glu Asp Arg Phe Tyr Lys
227      515      520      525
230 Ala Asn Arg Ala His Thr Tyr Leu Gly Asn Pro Ser Asn Ser Ser Glu
231      530      535      540
234 Ile Phe Pro Asp Met Leu Lys Phe Ala Glu Ala Cys Asp Ile Pro Ala
235 545      550      555      560
238 Ala Arg Val Thr Lys Val Ser Asp Leu Arg Ala Ala Ile Gln Thr Met
239      565      570      575
242 Leu Asp Thr Pro Gly Pro Tyr Leu Leu Asp Val Ile Val Pro His Gln
243      580      585      590
246 Glu His Val Leu Pro Met Ile Pro Ser Gly Ala Ala Phe Lys Asp Thr
247      595      600      605
250 Ile Thr Glu Gly Asp Gly
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254 <210> SEQ ID NO: 3
255 <211> LENGTH: 1930
256 <212> TYPE: DNA
257 <213> ORGANISM: Amaranthus hybridus
259 <400> SEQUENCE: 3
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264 cccagaaaag gttgcgatgt tctcgttgaa gctcttgaac gtgaagggtg taccgatggt      180

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266 tttgcttacc ctgggtggagc atccatggaa attcatcaag ctcttactcg ttctaataatc 240
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270 cgtgctactg gacgcgttg agtttgatt gccacttctg gtccagggtgc tactaatctt 360
272 gtttctggtc ttgctgatgc acttcttgac tcagtcctc ttgtcgccat tactgggcaa 420
274 gttccccggc gtatgattgg tactgatgct tttcaagaga ctccaattgt tgaggtaact 480
276 cgatccatta ccaagcataa ttatttggtg ttagatggtg aggatattcc tagaattggt 540
278 aaggaagctt tctttttagc taattctggt agacctggac ctgttttgat tgatattcct 600
280 aaagatattc agcaacaatt agttgttcct aattgggaac agcccattaa attgggtggg 660
282 tatctttcta gggtgcctaa acccacttat tctgctaatt aagagggact tcttgatcaa 720
284 attgtaaggt tagtgggtga gtctaagaga cctgtgctgt atactggagg tgggtgtttg 780
286 aattctagtg aagaattgag gaaatttgtc gaattgacag gtattccggt ggctagtact 840
288 ttaatggggt tgggggcttt cccttgact gatgatttat ctcttcatat gttgggaatg 900
290 cacgggactg tgtacgcgaa ttacgcggtt gataaggccg atttgttgct tgcttttggg 960
292 gttaggtttg atgatcgagt gactggttaag ctcgaggcgt ttgctagccg ggctaagatt 1020
294 gtgcacatcg atatcgattc tgctgaaatc gggaagaata agcaacctca tgtgtcgatt 1080
296 tgtggtgatg ttaaagtggc attacagggg ttgaataaga ttttgggaatc tagaaaagga 1140
298 aaggtgaaat tggatttctc taattggagg gaggagttga atgagcagaa aaagaagttt 1200
300 cctttgagtt ttaagacttt cggggatgca attcctccgc aatacgccat tcaggttctt 1260
302 gacgagttga cgaagggcga tgcggttgta agtactggtg ttgggcagca ccaaatgtgg 1320
304 gctgcccaat tctataagta ccgaaatcct cgccaatggc tgacctcggg tggtttgggg 1380
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310 agggtagaga atctcccgtt taaaatcatg ctcttgaaca atcaacattt aggtatggtt 1560
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316 gcagcccgtg ttaccaaggt gagcgattta agggctgcaa ttcaaacaat gttggatact 1740
318 ccaggaccgt atctgctgga tgtaatcgta ccacatcagg agcatgtgct gcctatgatt 1800
320 cctagcggtg ccgccttcaa ggacaccata acagagggtg atggaagaag ggcttattag 1860
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327 <210> SEQ ID NO: 4

328 <211> LENGTH: 619

329 <212> TYPE: PRT

330 <213> ORGANISM: Amaranthus hybridus

332 <400> SEQUENCE: 4

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338 Ile Thr Gln Ser Pro Ser Ser Leu Thr Asp Asp Lys Pro Ser Ser Phe
339 20 25 30
342 Val Ser Arg Phe Ser Pro Glu Glu Pro Arg Lys Gly Cys Asp Val Leu
343 35 40 45
346 Val Glu Ala Leu Glu Arg Glu Gly Val Thr Asp Val Phe Ala Tyr Pro
347 50 55 60
350 Gly Gly Ala Ser Met Glu Ile His Gln Ala Leu Thr Arg Ser Asn Ile
351 65 70 75 80
354 Ile Arg Asn Val Leu Pro Arg His Glu Gln Gly Gly Val Phe Ala Ala
355 85 90 95
358 Glu Gly Tyr Ala Arg Ala Thr Gly Arg Val Gly Val Cys Ile Ala Thr
359 100 105 110

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362 Ser Gly Pro Gly Ala Thr Asn Leu Val Ser Gly Leu Ala Asp Ala Leu
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366 Asp Asp Ser Val Pro Leu Val Ala Ile Thr Gly Gln Val Pro Arg Arg
367      130      135      140
370 Met Ile Gly Thr Asp Ala Phe Gln Glu Thr Pro Ile Val Glu Val Thr
371 145      150      155      160
374 Arg Ser Ile Thr Lys His Asn Tyr Leu Val Leu Asp Val Glu Asp Ile
375      165      170      175
378 Pro Arg Ile Val Lys Glu Ala Phe Phe Leu Ala Asn Ser Gly Arg Pro
379      180      185      190
382 Gly Pro Val Leu Ile Asp Ile Pro Lys Asp Ile Gln Gln Gln Leu Val
383      195      200      205
386 Val Pro Asn Trp Glu Gln Pro Ile Lys Leu Gly Gly Tyr Leu Ser Arg
387      210      215      220
390 Leu Pro Lys Pro Thr Tyr Ser Ala Asn Glu Glu Gly Leu Leu Asp Gln
391 225      230      235      240
394 Ile Val Arg Leu Val Gly Glu Ser Lys Arg Pro Val Leu Tyr Thr Gly
395      245      250      255
398 Gly Gly Cys Leu Asn Ser Ser Glu Glu Leu Arg Lys Phe Val Glu Leu
399      260      265      270
402 Thr Gly Ile Pro Val Ala Ser Thr Leu Met Gly Leu Gly Ala Phe Pro
403      275      280      285
406 Cys Thr Asp Asp Leu Ser Leu His Met Leu Gly Met His Gly Thr Val
407      290      295      300
410 Tyr Ala Asn Tyr Ala Val Asp Lys Ala Asp Leu Leu Leu Ala Phe Gly
411 305      310      315      320
414 Val Arg Phe Asp Asp Arg Val Thr Gly Lys Leu Glu Ala Phe Ala Ser
415      325      330      335
418 Arg Ala Lys Ile Val His Ile Asp Ile Asp Ser Ala Glu Ile Gly Lys
419      340      345      350
422 Asn Lys Gln Pro His Val Ser Ile Cys Gly Asp Val Lys Val Ala Leu
423      355      360      365
426 Gln Gly Leu Asn Lys Ile Leu Glu Ser Arg Lys Gly Lys Val Lys Leu
427      370      375      380
430 Asp Phe Ser Asn Trp Arg Glu Glu Leu Asn Glu Gln Lys Lys Lys Phe
431 385      390      395      400
434 Pro Leu Ser Phe Lys Thr Phe Gly Asp Ala Ile Pro Pro Gln Tyr Ala
435      405      410      415
438 Ile Gln Val Leu Asp Glu Leu Thr Lys Gly Asp Ala Val Val Ser Thr
439      420      425      430
442 Gly Val Gly Gln His Gln Met Trp Ala Ala Gln Phe Tyr Lys Tyr Arg
443      435      440      445
446 Asn Pro Arg Gln Trp Leu Thr Ser Gly Gly Leu Gly Ala Met Gly Phe
447      450      455      460
450 Gly Leu Pro Ala Ala Ile Gly Ala Ala Val Ala Arg Pro Asp Ala Val
451 465      470      475      480
454 Val Val Asp Ile Asp Gly Asp Gly Ser Phe Ile Met Asn Val Gln Glu
455      485      490      495
458 Leu Ala Thr Ile Arg Val Glu Asn Leu Pro Val Lys Ile Met Leu Leu

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VERIFICATION SUMMARY

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Input Set : A:\01640393aa.txt

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date